



Annual Reports :: Year 6 :: Ames Research Center

Team Reports: Ames Research Center

Ames Research Center
Executive Summary
Principal Investigator: David Des Marais

LINKING OUR ORIGINS TO OUR FUTURE

The Ames Research Center team maintains complementary lines of investigation designed to understand the context for habitable environments and life, the origins of life and its impact on the planetary environment, and the future of life in changing environments. The research addresses all seven goals of the new Astrobiology Roadmap and is formulated to address specific near-term objectives of the Roadmap in ways that link these objectives to flight missions and that also help to unify astrobiology. The Ames team conveys the content of its research program into its education and public outreach program through partnerships with the California Academy of Sciences (CAS), Yellowstone National Park (YNP), New York Hall of Science, and several K–14 educational organizations. Strong conceptual and functional links to multiple NASA missions provide context, motivation, and resource-sharing opportunities for both the research and the education and public outreach efforts.

We investigate the processes that control planetary formation in order to understand both the characteristics and the cosmic distribution of habitable environments

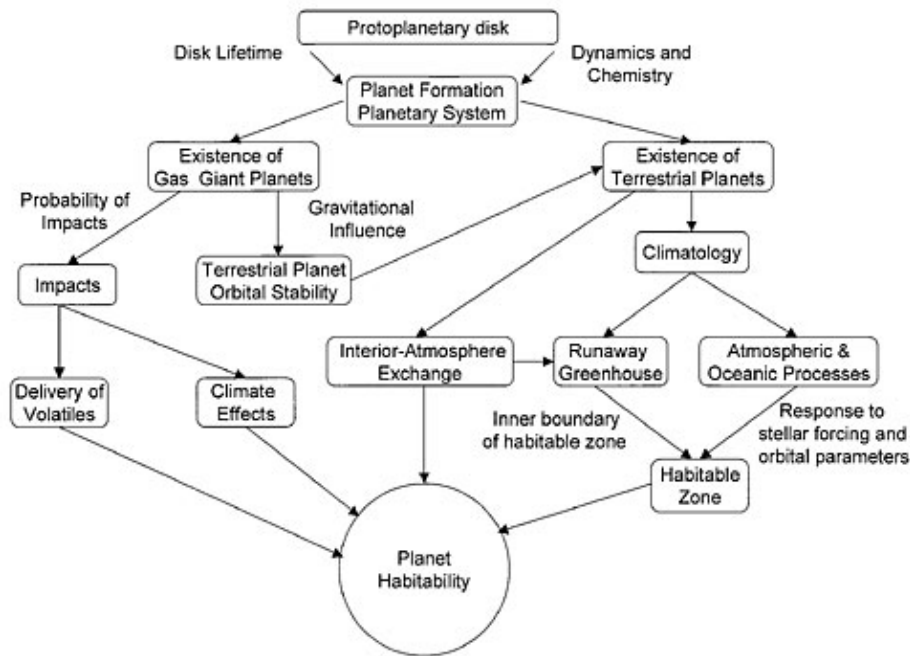


FIGURE 1 – Illustration of how processes act to determine planet habitability. These processes are of course a subset of all processes that have to be ultimately considered, but they are critical ones.

We modeled the evaporation of disks around low mass (solar-type) stars that is caused by external ultraviolet radiation from a nearby massive star. Photoevaporation can often affect the region where the giant planets form, at least in our solar system. Even terrestrial planets can be strongly affected. We are also investigating the dynamical viability of possible terrestrial planets orbiting in the habitable zones of known planet-bearing stars. Because a large amount of computing is required for models of these planets, and because public interest in both extrasolar planets and habitable worlds is intense, we are developing a distributed computing program along the lines of the seti@home model. We contributed a paper on the possible sources of turbulence that will enhance mixing and inter radial transfer in the protoplanetary nebula. We computed the migration of a condensation front; such a front might contribute to the rapid growth of gas giants such as Jupiter. A recently submitted manuscript documented that, for a sea surface temperature near 300 K, the clear sky upward longwave flux observed over the tropical Pacific Ocean exhibited the classic signature of the runaway greenhouse. We developed an analytical solution to the equations governing a runaway greenhouse, and found a region in flux and temperature space where two stable solutions exist. The “warm” solution can only be reached if a significant temperature perturbation occurs, such as a large impact. We are currently assessing the size of the impact required to produce a runaway greenhouse for a planet such as Mars.

We are tracing, spectroscopically and chemically, the cosmic evolution of organic molecules from the interstellar medium to protoplanetary disks, planetesimals, and finally onto habitable bodies. We also examine the abiotic mechanisms of primitive membrane formation under the primordial conditions

of a habitable planet. This work is complemented by astronomical observations and, ultimately, by analyses of cometary dust to be returned by the Stardust mission. We have completed studies of the infrared properties of neutral and ionized polycyclic aromatic hydrocarbons (PAHs) frozen in realistic interstellar water ice analogs. We have found a remarkable result. When frozen in water, PAHs are readily ionized and stabilized as ions as long as the ice is kept below about 50K. The spectra obtained during these studies will be used to interpret data taken with NASA's new Spitzer IR telescope. Also, we believe that we have detected evidence for deuterated PAHs in the interstellar medium, thus establishing an additional link between our ongoing lab studies of PAHs, including their photoproducts, and important biogenic species in meteorites. Finally we have studied the interstellar photostability of amino acids, nitriles, and precursor molecules in these ice analogs and compared photochemistry with proton bombardment processes.

We explore the origin of metabolism in the earliest ancestors of cells by testing the hypothesis that proteins might have arisen and initially evolved in the absence of a genome. Ultimately we will examine the evolutionary potential of an ensemble of proteins through theoretical and computational modeling. In prior years, we created, isolated, and identified a family of non-biological adenosine triphosphate (ATP)-binding proteins from an unconstrained random-sequence library. This past year, we performed multiple rounds of mRNA-display selection under increasingly denaturing conditions, in order to improve the folding stability of one of these proteins. We demonstrated that subsequent evolutionary optimization can readily yield sequence variants having improved folding and improved ligand binding. Using X-ray crystallography, we obtained the three-dimensional structure of an earlier protein variant that exhibited high affinity for ATP. The structure of our ATP binding protein reveals a new protein fold that has not been seen previously in biological proteins. This result supports the hypothesis that biological systems utilize only a subset of all possible protein folds. We developed and studied computationally a simple model of reaction (metabolic) networks catalyzed by functional proteins existing among random sequences. Networks can be classified into families (species) that persist even though individual networks disintegrate or transform with time. Relative populations of different families can change as environmental conditions change. Many phenomena, such as speciation, that operated in the context of genomic evolution might actually have evolved earlier in the absence of a genome. Ultimately, evolutionary progress of the systems was limited by the absence of a memory storage mechanism provided by the genome. Our findings thus support the hypothesis that initial protobiological evolution could have progressed without a genome but could not have reached the complexity approaching cellular systems as we know them today.

We are characterizing the major factors that govern the formation of potentially diagnostic biosignatures in microbial ecosystems. We documented further that marine hypersaline mats can be maintained in a relatively unchanged state in an Ames greenhouse facility under quasi *in situ* conditions. We have constructed a theoretical model predicting flows of substrate, and harvesting of energy, by various microbial guilds within the mat community. These models predict substantial production of volatile fatty acids and hydrogen, which we

have now also demonstrated experimentally. We have documented the diversity of Archaea within subtidal mats, with a particular emphasis on production of methane (as a volatile product of metabolism in photosynthetic systems). Detailed work has identified a novel methanogen in this system, and has documented the depth-dependence of methane production. We have identified an isoprenoid lipid that may serve as a biomarker characteristic of hypersaline environments. In collaboration with University of Colorado investigators, we documented the diversity of bacterial, archeal, and eukaryal domains within the subtidal mat system. This work expands the known division-level diversity of bacteria by about 40%, and has identified a novel eukaryote that branches at the kingdom level. We identified and characterized a series of spring systems hosted in northern California ophiolites. At one site, we demonstrated that serpentinization, a rock alteration reaction that yields the potential biological substrate H_2 , is active at the relatively low temperatures encountered by this ophiolite during its 100-Myr history, but that the process of alteration of these rocks is still not yet complete.

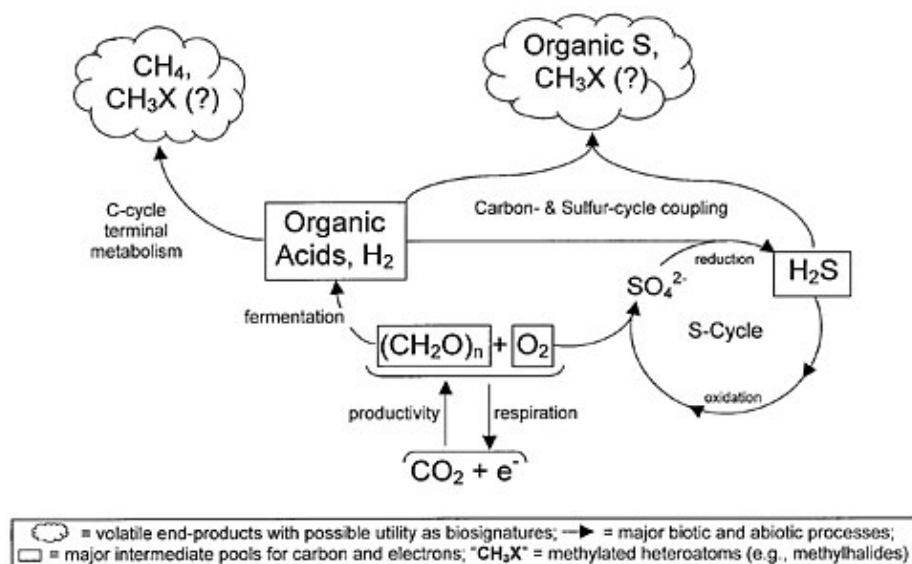


FIGURE 2 – Major steps in the anaerobic transformation of photosynthetic productivity. This approach quantifies the flow of carbon and electrons fixed by primary productivity through each of the major processes and reservoirs identified in this diagram. Molecular biology and organic biomarker approaches are used to characterize the organisms that mediate the transformation process. At major "junction points", where carbon or electrons may have alternate fates (e.g., H_2 /Organic Acid or H_2S pools), we characterize the micro- and macro-environmental factors that regulate their ultimate partitioning into the spectrum of biomarker end-products.

We extend the ecosystem-level studies of photosynthetic microbial mats to a planetary scale by refining and evaluating quantitative models that simulate energy relationships, biogeochemical cycling, trace gas exchange, and biodiversity in these systems. We refined and submitted for publication our model of hypersaline mats to Microbial BioGeoChemistry. We ran sensitivity tests to answer outstanding questions about the relative diel changes in the rates of sulfate respiration and dissimilatory sulfate reduction. We found that

cyanobacterial fermentation is critical in supplying H_2 for dissimilatory sulfate reduction, and that nighttime sulfur oxidation in colorless sulfur bacteria is critical in supplying S^0 for cyanobacterial fermentation. These findings have consequences for further development of the carbon cycle component of our model, which will include organic carbon and methanogenesis. The model will address the precursors of methylamines, which can be utilized for methane production. The current challenge is to find or model pool sizes of these precursors, which include critical osmoregulators in these hypersaline ecosystems.

We have examined the effects of climate variability on a vegetation-rich biosphere over intermediate time scales, using South American ecosystems as a model. We continue to develop a predictive Paleo-Net Primary Productivity model for South America, using the output of the NASA-CASA model for 41 sites in South America. Comprehensive modern solar irradiance data have recently become available, and such data play an important role as drivers in our model. We are currently exploring potential proxies of solar irradiance in the fossil record. We are also using modern temperature and precipitation data in the model, proxies for which are found in fossil pollen and tree-rings. With Dr. Jorge Marcos, we are establishing the observation bases for intensive studies in Ecuador. We are investigating additional field sites in South America for testing our model.

We are assessing the potential for life to move beyond its planet of origin, as a potentially important component in the evolution of life in our own solar system. We have begun work on an extremely halophilic alga, *Dunaliella salina*, to test for radiation resistance. We are investigating meteorites with exceptionally large cracks as model vehicles for the interplanetary transport of microbes. We are collaborating with investigators at the DLR (German space agency) who have designed and built a chamber to simulate the conditions that microbial samples will encounter in Earth orbit. The DLR has designed and built a sample holding rack that is a duplicate of the flight rack. We demonstrated that the rack materials will not harm our microbial samples and that samples will not suffer cross contamination. We determined the maximum and minimum temperatures that samples could withstand during pre-launch, launch, during the test, and still be returned without being harmed. Results indicated that 50°C is the upper temperature limit. No deleterious effects could be detected within samples that were held at -25°C for 3 months.

We have further developed our partnerships with the California Academy of Sciences, Yellowstone National Park, and the New York Hall of Science to develop new astrobiology workshops, activities, exhibits, and other products. CAS has chosen to utilize astrobiology to link its natural history museum, planetarium, and aquarium under the theme, "Earth and its Place in the Universe." Ames personnel contributed substantial content and images to astrobiology exhibits that the CAS now displays at their newly occupied temporary campus on Howard Street in San Francisco. Ames and CAS are continuing to develop materials for future exhibits at the Howard Street site, as well as concepts for displays at the permanent site at Golden Gate Park.



FIGURE 3 – Ames team members tour California Academy of Sciences to see the new astrobiology exhibits currently on display at their newly opened temporary campus on Howard Street in San Francisco. The Ames team made significant contributions to these exhibits by submitting numerous images, captions, and content relating to astrobiology and the current research in work throughout the team.

The Ames partnership with Yellowstone National Park utilizes the important role that the Park's thermal features have regarding studies of both the early evolution of life on Earth and the search for evidence of habitable environments and life on Mars. This past year Ames contributed a book chapter on microbiology and ecology to the 2004 edition of the Yellowstone Resources and Issues Guide. The Ames team contributed considerable astrobiology content for new trailside interpretive signs. This astrobiology sign project is currently in final review at Yellowstone, with sign development and production scheduled to begin during the summer of 2004. Ultimately, astrobiology will be integrated into permanent exhibits for the major visitor centers. Working with Lockheed–Martin Space Projects Corporation and with NAI Central, the Ames team has facilitated the donation of substantial funds to the Yellowstone Foundation, as a key part of the program to develop interpretive products that disseminate astrobiology and Yellowstone to the general public.



FIGURE 4 – Volcanic activity has interacted with water on Mars, as well as on Earth. Thermal springs like the Grand Prismatic Spring at Midway Geyser Basin, in Yellowstone National Park, are natural oases for diverse life forms, and hot spring mineral deposits can preserve fossils. Yellowstone's natural wonders thus guide our search for evidence of ancient martian thermal springs, and potentially, for traces of martian life. The public's fascination with Yellowstone creates an opportunity to transfer the excitement of Mars exploration to its visitors.

The Ames team continues to work with TERC, Cambridge, MA , to apply its new astrobiology curriculum to a broad array of education and outreach projects.

The Ames team has established a substantial presence on current NASA missions. The Ames team Principal Investigator serves as one of the leads for strategic planning on the Science Operations Working Group of the Mars Exploration Rover mission. Another team member serves as a co-investigator with the Kepler mission of NASA's Discovery program. Several team members are involved with missions that are scheduled and planned missions for the next several years.